

Application No.: NOT YET ASSIGNED

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Original) An array in which different kinds of biosubstances obtained from an organism of interest, or synthetic substances interacting with such biosubstances are arranged and immobilized on a support in an orderly manner,

the different kinds of biosubstances or the synthetic substances being arranged such that a chromosomal order of base sequence blocks corresponding to the biosubstances is ascertainable.

2. (Original) An array as set forth in claim 1, wherein at least part of the different kinds of biosubstances or the synthetic substances are arranged in the chromosomal order of the base sequence blocks corresponding to the biosubstances.

3. (Currently Amended) An array as set forth in claim 1 ~~or 2~~, wherein the support includes a label that indicates the chromosomal order of the base sequence blocks corresponding to the biosubstances.

4. (Original) An array as set forth in claim 1,
wherein the biosubstances or the synthetic substances immobilized on the support each include sequence position information corresponding to the chromosomal order of the base sequence blocks corresponding to the biosubstances, and

wherein, in use, data is acquired and the sequence position information is read out, so as to rearrange sequences of the data in the chromosomal order.

5. (Original) An array as set forth in claim 1,
wherein the support comprises a collection of micro supports on which the biosubstances or the synthetic substances are individually immobilized,

Application No.: NOT YET ASSIGNED

wherein the micro supports each include sequence position information corresponding to the chromosomal order of the base sequence blocks corresponding to the biosubstances, and

wherein sequences of acquired data are rearranged in the chromosomal order based on the sequence position information.

6. (Currently Amended) An array as set forth in ~~any one of claim[[s]] 1 through 5~~, wherein the biosubstances comprise nucleic acids or polypeptides.

7. (Original) An array as set forth in claim 6, wherein the nucleic acid comprises DNA.

8. (Original) An array as set forth in claim 7, wherein the DNA comprises a genetic marker, genomic DNA, genomic DNA treated with a restriction enzyme, cDNA, EST, or synthetic oligoDNA.

9. (Currently Amended) An array as set forth in claim 7 ~~or 8~~, wherein the DNA immobilized on the support is arranged based on a genetic map or physical map.

10. (Currently Amended) An array as set forth in ~~any one of claim[[s]] 7 through 9~~, wherein genomic DNA treated with a restriction enzyme is used as target DNA.

11. (Original) An array as set forth in claim 10, wherein the target DNA is fractionated by size after the treatment with a restriction enzyme.

12. (Currently Amended) An array as set forth in ~~any one of claim[[s]] 1 through 5~~, wherein the polypeptides comprise proteins, fragments of protein, or oligopeptides.

13. (Original) An array as set forth in claim 12, wherein the proteins comprise enzymes, kinase, antibodies, receptors, or proteins with SH3 region.

Application No.: NOT YET ASSIGNED

14. (Currently Amended) An array as set forth in claim 12 ~~or 13~~, wherein the proteins immobilized on the support are arranged based on a genetic map or physical map.

15. (Currently Amended) An array as set forth in ~~any one of claim[[s]] 1 through 14~~, wherein the support or micro support comprises an inorganic substrate, an organic film, or a bead.

16. (Currently Amended) An array as set forth in ~~any one of claim[[s]] 1 through 15~~, which comprises any one of a micro array, a macro array, a bead array, and a protein chip.

17. (Original) A producing process of an array, comprising the step of orderly arranging and immobilizing on a support different kinds of biosubstances obtained from an organism of interest, or synthetic substances interacting with such biosubstances,

said step comprising arranging and immobilizing the biosubstances or the synthetic substances according to the order in which genes corresponding to the biosubstances are coded for on a chromosome of the organism.

18. (Original) A producing process as set forth in claim 17, wherein the biosubstances comprise nucleic acids or polypeptides.

19. (Currently Amended) A genotype identification method, comprising identifying a target trait-including chromosome fragment, using the array of ~~any one of claim[[s]] 7 through 11~~, from hybrids obtained by crossing organisms.

20. (Original) An identification method as set forth in claim 19, wherein the organisms comprise laboratory animals and plants.

Application No.: NOT YET ASSIGNED

21. (Original) A gene diagnosis method for identifying human genotypes, using the identification method of claim 20.

22. (Currently Amended) A screening method for screening for a target trait-carrying variety from hybrids obtained by crossing organisms whose characteristics are to be improved, using the array of ~~any one of claim[[s]] 7 through 11~~.

23. (Original) A screening method as set forth in claim 22, wherein the living organisms crossed for variety improvement comprise laboratory animals and plants, domestic animals, or crops.

24. (Original) A screening method as set forth in claim 23, wherein the crops comprise cereals.

25. (Original) A screening method as set forth in claim 24, wherein the cereals comprise rice, wheat, corn, or barley.

26. (Currently Amended) A genotype analyzing and display system, comprising:
genotype origin detecting means for comparing (a) gene expression level information and polymorphism information comprehensively obtained through a hybridization analysis of hybrid individuals with the array of ~~any one of claim[[s]] 7 through 11~~ with (b) genetic information of parents of the hybrid individuals, and a genetic map of a species to which the hybrid individuals belong, so as to determine whether a genotype of a hybrid individual of interest derives from which parent; and

display information generating means for gathering a plurality of results obtained from the genotype origin detecting means and, based on the results, generating display information used to display a plurality of genotypes altogether on a chromosome basis, so as to determine whether individual genotypes derives from which parent.

Application No.: NOT YET ASSIGNED

27. (Currently Amended) A quantitative loci analyzing system which uses the array of ~~any one of claim[[s]] 7 through 11~~, and in which a genetic marker of a species of interest is immobilized on the array,

said quantitative loci analyzing system comprising:

genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing the array with a genomic sample obtained from the hybrid individuals of a certain hybrid line with (b) a genetic map of a species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line; and

quantitative loci detecting means for detecting a quantitative locus of a phenotype of interest of the hybrid individual, by confirming whether a phenotypic value indicative of the phenotype is linked to the genetic marker.

28. (Currently Amended) A gene interaction analyzing system which uses the array of ~~any one of claim[[s]] 7 through 11~~, and in which a genetic marker of a species of interest is immobilized on the array,

said gene interaction analyzing system comprising:

genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing the array with a genomic sample obtained from the hybrid individuals of a certain hybrid line (b) with a genetic map of species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line;

spot marker information generating means for comparing the specified genetic marker with the genetic marker immobilized on the support, so as to generate spot marker information, being genetic marker information for use in analysis, from hybridization results obtained from individual spots on the array; and

Application No.: NOT YET ASSIGNED

hereditary factor specifying means for specifying, with regard to an arbitrarily selected phenotype and gene to be analyzed, a hereditary factor of the selected phenotype by determining whether the phenotypic value indicative of the phenotype, and an expressed gene included in expression profile information obtained from the hybrid individual are linked to a plurality of spot marker information.

29. (Original) A genotype analyzing and display system, comprising:

genotype origin detecting means for comparing (a) gene expression level information and polymorphism information comprehensively obtained through a hybridization analysis of hybrid individuals using a nucleic acid array with (b) genetic information of parents of the hybrid individuals, and a genetic map of species to which the hybrid individuals belong, so as to determine whether a genotype of a hybrid individual of interest derives from which parent; and

display information generating means for gathering a plurality of results obtained from the genotype origin detecting means and, based on the results, generating display information used to display a plurality of genotypes altogether on a chromosome basis, so as to determine whether individual genotypes derives from which parent.

30. (Original) A genotype analyzing and display system as set forth in claim 29, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

31. (Currently Amended) A genotype analyzing and display system as set forth in claim 29 ~~or 30~~, further comprising genetic map constructing means for constructing, based on genetic map constructing information, a genetic map of a species to which the hybrid individuals belong.

32. (Original) A genotype analyzing and display system as set forth in claim 31, wherein

Application No.: NOT YET ASSIGNED

the genetic map constructing information comprises names of genes and/or genetic markers known in the species, and chromosomal loci of the genes and/or genetic markers.

33. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 32~~, wherein the genotype origin detecting means determines a genotype as being homozygous for one of the parents, heterozygous, or unrecognizable to yield a result.

34. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 32~~, wherein the genotype origin detecting means uses genotype information and/or gene expression profile information of parents as genetic information of parents.

35. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 34~~, wherein the display information generating means generates display information including at least one of recombination number and recombination frequency of individual chromosomes.

36. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 35~~, wherein the display information generating means generates display information such that an origin of a genotype is identifiable based on different display colors or patterns.

37. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 36~~, comprising at least one of input means and output means.

Application No.: NOT YET ASSIGNED

38. (Original) A genotype analyzing and display system as set forth in claim 37, wherein the input means receives at least one of comprehensive expression level information of genes of the hybrid individuals, and genetic information of parents.

39. (Original) A genotype analyzing and display system as set forth in claim 38, wherein the input means receives genetic map constructing information.

40. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 37 through 39~~, comprising:

image reading means, provided as the input means, for enabling a hybridization result of the nucleic acid array to be read out as image information; and

image information processing means for analyzing an expression level of gene based on the image information and generating comprehensive expression level information of gene.

41. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 37 through 40~~, comprising manual input means, provided as the input means, for modifying at least one of: the comprehensive expression level information of gene of the hybrid individuals; the genetic information of parents; and the genetic map constructing information.

42. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 37 through 41~~, wherein the output means comprises at least one of: image display means for displaying the display information on a screen; and printing means for printing the display information.

43. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 37 through 41~~, wherein the input means and the output means comprise

Application No.: NOT YET ASSIGNED

external information input-output means for sending and receiving information to and from an external device.

44. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 43~~, wherein the nucleic acid array comprises a DNA array on which DNA is immobilized.

45. (Original) A genotype analyzing and display system as set forth in claim 44, wherein the DNA immobilized on the DNA array comprises a genetic marker, genomic DNA, genomic DNA treated with a restriction enzyme, cDNA, EST, or synthetic oligoDNA.

46. (Currently Amended) A genotype analyzing and display system as set forth in ~~any one of claim[[s]] 29 through 45~~, which comprises any one of a micro array, a macro array, and a bead array.

47. (Currently Amended) A genotype identification method, comprising identifying a target trait-including chromosome fragment, using the genotype analyzing and display system of ~~any one of claim[[s]] 29 through 46~~, from hybrids obtained by crossing organisms.

48. (Original) An identification method as set forth in claim 47, wherein the organisms comprise laboratory animals and plants.

49. (Currently Amended) A screening method for screening for a target trait-carrying variety from hybrids obtained by crossing organisms whose characteristics are to be improved, using the genotype analyzing and display system of ~~any one of claim[[s]] 29 through 46~~.

50. (Original) A screening method as set forth in claim 49, wherein the organisms crossed for variety improvement comprise laboratory animals and plants, domestic animals, or

Application No.: NOT YET ASSIGNED

crops.

51. (Original) A quantitative loci analyzing system, comprising:
genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing a genomic sample of the hybrid individuals of a certain hybrid line with a nucleic acid array on which a genetic marker of a species of interest is immobilized with (b) a genetic map of a species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line; and quantitative loci detecting means for detecting a quantitative locus of a phenotype of interest of the hybrid individual, by confirming whether a phenotypic value indicative of the phenotype is linked to the genetic marker.

52. (Original) A quantitative loci analyzing system as set forth in claim 51, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

53. (Currently Amended) A quantitative loci analyzing system as set forth in claim 51 ~~or 52~~, further comprising genetic map constructing means for constructing, based on genetic map constructing information, a genetic map of a species to which the hybrid individuals belong.

54. (Original) A quantitative loci analyzing system as set forth in claim 53, wherein the genetic map constructing information comprises names of genes and/or genetic markers known in the species, and chromosomal loci of the genes and/or genetic markers.

55. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 54~~, wherein the genetic marker information used by the genetic marker specifying means comprises a genetic marker with polymorphism.

Application No.: NOT YET ASSIGNED

56. (Original) A quantitative loci analyzing system as set forth in claim 55, wherein the genetic marker comprises SNP or RFLP.

57. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 56~~, wherein the quantitative loci detecting means detects a quantitative locus of phenotype by interval mapping.

58. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 57~~, comprising:

image reading means for enabling a hybridization result of the nucleic acid array to be read out as image information; and

image information processing means for analyzing the image information and generating comprehensive expression level information of gene.

59. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 57~~, comprising at least one of input means and output means.

60. (Original) A quantitative loci analyzing system as set forth in claim 59, wherein the input means receives at least one of the genetic marker information and the phenotypic value.

61. (Original) A quantitative loci analyzing system as set forth in claim 60, wherein the input means receives at least one of the genetic map and the genetic map constructing information.

62. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 59 ~~through 61~~, comprising manual input means, provided as the input means, for

Application No.: NOT YET ASSIGNED

modifying at least one of: the comprehensive presence information of gene of the hybrid individuals; the genetic marker information, and the genetic map constructing information.

63. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 59 ~~through 62~~, wherein the output means comprises at least one of image display means for displaying an analysis result on a screen; and printing means for printing an analysis result.

64. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 59 ~~through 63~~, wherein the input means and the output means comprise external information input-output means for sending and receiving information to and from an external device.

65. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 64~~, wherein the nucleic acid array comprises a DNA array on which DNA is immobilized.

66. (Currently Amended) A quantitative loci analyzing system as set forth in ~~any one of~~ claim[[s]] 51 ~~through 65~~, wherein the nucleic acid array comprises a micro array, a macro array, or a bead array.

67. (Currently Amended) A quantitative trait analyzing method for analyzing a quantitative trait of an organism, using the quantitative loci analyzing system of ~~any one of~~ claim[[s]] 51 ~~through 66~~.

68. (Currently Amended) A gene searching method for searching for a gene associated with expression of a trait of interest, using the quantitative loci analyzing system of ~~any one of~~ claim[[s]] 51 ~~through 66~~.

Application No.: NOT YET ASSIGNED

69. (Currently Amended) A variety improvement method for organisms, which uses the quantitative loci analyzing system of ~~any one of claim[[s]] 51 through 66~~.

70. (Original) A variety improvement method as set forth in claim 69, wherein the organisms comprise laboratory animals and plants, domestic animals, or crops.

71. (Original) A gene interaction analyzing system, comprising:
genetic marker specifying means for comparing (a) comprehensive presence information of genes of hybrid individuals, obtained by hybridizing a genomic sample of the hybrid individuals of a certain hybrid line with a nucleic acid array on which a genetic marker of a species of interest is immobilized with (b) a genetic map of a species to which the hybrid individuals belong, and genetic marker information known in the species, so as to specify a genetic marker that exists in the hybrid line;

spot marker information generating means for comparing the specified genetic marker with the genetic marker immobilized on the nucleic acid array, so as to generate spot marker information, being genetic marker information for use in analysis, from hybridization results obtained from individual spots on the nucleic acid array; and

hereditary factor specifying means for specifying, with regard to an arbitrarily selected phenotype and gene to be analyzed, a hereditary factor of the selected phenotype by determining whether the phenotypic value indicative of the phenotype, and an expressed gene included in expression profile information obtained from the hybrid individual are linked to a plurality of spot marker information.

72. (Original) A gene interaction analyzing system as set forth in claim 70, wherein the nucleic acid array comprises a chromosomal location recognizable array in which a plurality of nucleic acid molecules immobilized thereon are arranged such that a chromosomal order of base sequence blocks corresponding to the nucleic acid molecules is ascertainable.

Application No.: NOT YET ASSIGNED

73. (Currently Amended) A gene interaction analyzing system as set forth in claim 71 ~~or 72~~, further comprising genetic map constructing means for constructing, based on genetic map constructing information, a genetic map of a species to which the hybrid individuals belong.

74. (Original) A gene interaction analyzing system as set forth in claim 73, wherein the genetic map constructing information comprises names of genes and/or genetic markers known in the species, and chromosomal loci of the genes and/or genetic markers.

75. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 74~~, wherein the genetic marker information used by the genetic marker specifying means comprises a genetic marker with polymorphism.

76. (Original) A gene interaction analyzing system as set forth in claim 75, wherein the genetic marker comprises SNP or RFLP.

77. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 76~~, wherein the spot marker information generating means generates spot marker information only for a genetic marker spot found by hybridization.

78. (Original) A gene interaction analyzing system as set forth in claim 77, wherein the spot marker information generating means generates spot marker information by including position information of a genetic marker immobilized on the nucleic acid array.

79. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 78~~, comprising expression profile information generating means for analyzing an expression profile in regard to a comprehensive gene expression level obtained

Application No.: NOT YET ASSIGNED

from the hybrid individual, so as to generate expression profile information of the hybrid individual.

80. (Original) A gene interaction analyzing system as set forth in claim 79, wherein the expression profile information generating means generates expression profile information of the hybrid individual by comprehensively measuring gene expression, using at least one of a micro array, a macro array, a bead array, and a differential display.

81. (Original) A gene interaction analyzing system as set forth in claim 80, wherein the expression profile information generating means generates expression profile information using a nucleic acid array used to obtain comprehensive presence information of gene of the hybrid individual, or a nucleic acid array on which the same sample has been spotted.

82. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 81~~, wherein the nucleic acid array comprises a DNA array on which DNA is immobilized.

83. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 82~~, wherein the nucleic acid array comprises a micro array, a macro array, or a bead array.

84. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 83~~, wherein the hereditary factor specifying means specifies a hereditary factor of a phenotype based on a quantitative trait locus (QTL) that exists among genetic markers obtained by interval mapping.

85. (Original) A gene interaction analyzing system as set forth in claim 84, wherein the hereditary factor specifying means uses information of expression level of a gene associated with the genetic marker, so as to specify a hereditary factor of the phenotype.

Application No.: NOT YET ASSIGNED

86. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 71 ~~through 85~~, comprising at least one of input means and output means.

87. (Original) A gene interaction analyzing system as set forth in claim 86, wherein the input means receives at least one of: comprehensive presence information of gene of the hybrid individual; the genetic marker information; the phenotypic value; and the expression profile information.

88. (Original) A gene interaction analyzing system as set forth in claim 87, wherein the input means receives at least one of the genetic map and the genetic map constructing information.

89. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 86 ~~through 88~~, comprising:

image reading means, provided as the input means, for enabling a hybridization result of the nucleic acid array to be read out as image information; and

image information processing means for analyzing an expression level of gene based on the image information and generating comprehensive expression level information of gene.

90. (Original) A gene interaction analyzing system as set forth in claim 89, wherein the input means receiving the expression profile information comprises image information reading means.

91. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of~~ claim[[s]] 86 ~~through 90~~, comprising manual input means, provided as the input means, for modifying at least one of: the comprehensive presence information of gene of the hybrid individuals; the genetic marker information, and the genetic map constructing information.

Application No.: NOT YET ASSIGNED

92. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of claim[[s]] 86 through 91~~, wherein the output means comprises at least one of image display means for displaying an analysis result on a screen; and printing means for printing an analysis result.

93. (Currently Amended) A gene interaction analyzing system as set forth in ~~any one of claim[[s]] 86 through 92~~, wherein the input means and the output means comprise external information input-output means for sending and receiving information to and from an external device.

94. (Currently Amended) A gene interaction analyzing method for analyzing interaction between genes, using the gene interaction analyzing system of ~~any one of claim[[s]] 71 through 93~~.

95. (Currently Amended) A gene searching method for searching for a gene associated with a trait of interest, using the gene interaction analyzing system of ~~any one of claim[[s]] 71 through 93~~.

96. (Currently Amended) A variety improvement method for organisms, which uses the gene interaction analyzing system of ~~any one of claim[[s]] 71 through 93~~.

97. (Original) A variety improvement method as set forth in claim 96, wherein the organisms comprise laboratory animals and plants, domestic animals, or crops.